

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 14:06:59 ; Search time 562 Seconds
(without alignments)
10263.124 Million cell updates/sec

Title: US-10-018-105-3
Perfect score: 3525
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Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:
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6: /cgn2.6/prodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2155.2	61.1	2358	US-09-248-796A-6328	Sequence 6328, Ap
2	423.8	12.0	507	US-09-248-796A-6327	Sequence 6327, Ap
c	168.2	4.8	537	US-08-998-416-66	Sequence 66, Appl
4	118.2	3.4	2445	US-09-248-796A-6302	Sequence 6302, Ap
5	73.4	2.1	708	US-09-248-796A-10622	Sequence 10622, A
6	71.8	2.0	19124	US-08-487-826B-13	Sequence 13, Appl
7	68.8	2.0	1141	US-09-806-708B-22	Sequence 22, Appl
8	68	1.9	767677	US-09-949-016-12147	Sequence 12147, A
9	68	1.9	767677	US-09-949-016-17361	Sequence 17361, A
c	10	67.6	1.9	29717	Sequence 17361, A
c	11	67.6	1.9	60376	Sequence 16284, A
c	12	66.8	1.9	14066	Sequence 12423, A
c	13	66.4	1.9	19438	Sequence 56, Appl
c	14	66	1.9	26000	Sequence 12699, A
c	15	65.8	1.9	205044	Sequence 10, Appl
c	16	65.8	1.9	205044	Sequence 15851, A
c	17	65.8	1.9	205044	Sequence 15852, A
c	18	65.8	1.9	223471	Sequence 15853, A
c	19	65.8	1.9	223471	Sequence 12387, A
c	20	65.8	1.9	223471	Sequence 12724, A
c	21	65.2	1.8	1037	Sequence 12725, A
c	22	65.2	1.8	1159	Sequence 3, Appl
c	23	65.2	1.8	1471	Sequence 1, Appl
c	24	65	1.8	18773	Sequence 2, Appl
c	25	64	1.8	1141	Sequence 14164, A
c	26	63.6	1.8	119153	Sequence 22, Appl
c	27	63.4	1.8	837	Sequence 12378, A
					Sequence 288, App

ALIGNMENTS

RESULT 1

US-09-248-796A-6328
; Sequence 6328, Application US/09248796A
; Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 6328

LENGTH: 2358

TYPE: DNA

ORGANISM: Candida albicans

US-09-248-796A-6328

Query Match 61.1%; Score 2155.2; DB 4; Length 2358;

Best Local Similarity 97.2%; Pred. No. 0; Mismatches 23; Indels 44; Gaps 8;

Matches 2293; Conservative 0

QY 285 ATAAATATAATTAAGAGTATATCTCCCTTTTGTGTTTTTTTTTTTCCAGCCATGTCGG 344

Db 1 ATAAATATAATTAAGAGTATATCTCCCTTTTGTGTTTTTTTTTTTCCAGCCATGTCGG 58

QY 345 ATAGTGAAGTATTATCAAAATCACTACTAATCAACCTATTCCTAGATCTGATGAAG 404

Db 59 ATAGTGAAGTATTATCAAAATCACTACTAATCAACCTATTCCTAGATCTGATGAAG 118

QY 405 TATTGGATGATCATAGAAATCAAAATCACTACTAATCAACCTATTCCTAGATCTGATGAAG 464

Db 119 TATTGGATGATCATAGAAATCAAAATCACTACTAATCAACCTATTCCTAGATCTGATGAAG 178

QY 465 AGTTGGAATTAATAATCAGAAATCAGAAATCAGAAATCAGAAATCAGAAATCAGAAAT 512

Db 179 AGTTGGAATTAATAATCAGAAATCAGAAATCAGAAATCAGAAATCAGAAATCAGAAAT 238

QY 513 AACAAACAACATCATCAAGAGATTATCATCAGATAATGCTTAAACATTCGTAAT 572

Db 239 AACAAACAACATCATCAAGAGATTATCATCAGATAATGCTTAAACATTCGTAAT 298

QY 573 CTGGTTCTTCAATTAAGAAAAATCTATCTTACCGATAAGATAGATTACCAACCTTA 632

Db 299 CTGGTTCTTCAATTAAGAAAAATCTATCTTACCGATAAGATAGATTACCAACCTTA 358

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OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 13:36:05 ; Search time 1739 Seconds
(without alignments)
11999.476 Million cell updates/sec

Title: US-10-018-105-3
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: Geneseq1990a.*
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- 7: Geneseq2002bs.*
- 8: Geneseq2003a.*
- 9: Geneseq2003bs.*
- 10: Geneseq2003cs.*
- 11: Geneseq2003ds.*
- 12: Geneseq2004a.*
- 13: Geneseq2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3523	99.9	3525	3 AAC87954	Aac87954 Candida a
2	2769	78.6	2769	6 AB232388	Abz32388 Candida a
3	263.8	7.5	684	6 ABN21722	Abn21722 Human ORF
4	179.6	5.1	1992	8 ABT19393	Abt19393 Aspergill
5	179.6	5.1	1992	8 ABT21213	Abt21213 Aspergill
6	169.4	4.8	860	8 ABZ51492	Abz51492 Aspergill
7	168.2	4.8	537	2 ADRO1374	Adr01374 A. gosyp
8	118	3.3	462	6 ABN76186	Abn76186 Human gly
9	117.6	3.3	8056	8 ABZ10246	Abz10246 Haematopo
10	116.4	3.3	688	3 AAF14580	Aaf14580 Aspergill
11	113.6	3.2	2048	8 ABT18799	Abt18799 Aspergill
12	113.6	3.2	2048	8 ABT18205	Abt18205 Aspergill
13	113.6	3.2	4048	8 ABT20019	Abt20019 Aspergill
14	113.6	3.2	4048	8 ABT20019	Abt20019 Aspergill
15	113.6	3.2	7990	13 ADP84473	Adp84473 Aspergill
16	107.8	3.1	321	6 ABN22505	Abn22505 Human ORF
17	106.8	3.0	4985	6 ABQ75107	Abq75107 Anopheles
18	106.8	3.0	4985	10 ACF79720	Acf79720 Mosquito
19	106.2	3.0	575	3 AAF07924	Aaf07924 Fusarium
20	94.4	2.7	969	6 ABQ39490	Abq39490 Oligonuc

21	94.4	2.7	969	6 ABQ39491	Abq39491 Oligonuc
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23	90	2.6	3996	6 AAD47004	Aad47004 Plasmodiu
24	86.6	2.5	8056	8 ABZ10100	Abz10100 Haematopo
25	85.8	2.4	2000	10 ADK62467	Adk62467 Disease t
26	84.8	2.4	8056	8 ABZ10100	Abz10100 Haematopo
27	84	2.4	7676	6 ABL34598	Ab134598 Human met
28	84	2.4	7676	6 ABL70409	Ab170409 Chemical
29	84	2.4	7676	7 ADS99859	AdS99859 Bisulphit
30	81.2	2.3	4985	6 ABQ75107	Abq75107 Anopheles
31	81.2	2.3	4985	10 ACF79720	Acf79720 Mosquito
32	79.8	2.3	6033	3 AAA70152	Aaa70152 Plasmodiu
33	79.8	2.3	9859	13 ADS89440	AdS89440 Oligonuc
34	79.8	2.3	9859	13 ADS89714	AdS89714 Oligonuc
35	79.6	2.3	3931	9 ACC84661	Acc84661 P. faicip
36	78.2	2.2	8759	8 ABZ10238	Abz10238 Haematopo
37	78.2	2.2	8759	8 ABZ09964	Abz09964 Haematopo
38	78.2	2.2	8759	8 ABZ10092	Abz10092 Haematopo
39	78.2	2.2	8759	8 ABZ10110	Abz10110 Haematopo
40	78.2	2.2	8759	10 ADB54086	AdB54086 Pretreate
41	78.2	2.2	8759	10 ADB54214	AdB54214 Pretreate
42	78.2	2.2	8759	10 ADE84072	AdE84072 Human lym
43	78.2	2.2	8759	10 ADE84148	AdE84148 Human lym
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45	78.2	2.2	8759	13 ADS89240	AdS89240 Oligonuc

ALIGNMENTS

RESULT 1
AAC87954
ID AAC87954 standard; DNA; 3525 BP.
AC AAC87954;
XX

DT 06-MAR-2001 (first entry)

DE Candida albicans CaALR1 nucleotide sequence.

KW Candida albicans; yeast pathogen; identification; fungal; antifungal;
KW CaKRES; CaALR1; CaCDC24; diagnosis; fungicide; fungal infection; ds.
XX

OS Candida albicans.

XX WO2000068420-A2.
XX

PD 16-NOV-2000.

XX 05-MAY-2000; 2000WO-CA000533.
XX

XX 05-MAY-1999; 99US-0132878P.
XX

XX (MYCO-) MYCOTA BIOSCIENCES INC.
XX

XX Roemer T, Bussey H, Davison J;
XX

XX WPI; 2000-687652/67.
XX

XX P-PSDB; AAB36515.
XX

XX New DNA encoding essential proteins of Candida albicans, useful for
XX diagnosing fungal infections and to screen for clinical or agricultural
XX antifungal agents.

XX Claim 3; Fig 2A; 76pp; English.

XX The present sequence represents the fungus-specific Candida albicans gene
XX CaALR1. The present invention describes the fungus-specific genes CaKRES,
XX CaALR1 and CaCDC24 isolated in the yeast pathogen C. albicans. The genes
XX have antifungal and fungicide activity. The genes in C. albicans and are
XX useful as drug targets. Fragments of them are useful as probes and
XX primers for diagnosis of fungal infections, also as antisense and
XX ribozyme agents. Proteins encoded by the genes are used to screen for

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OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 13:38:30 ; Search time 14937 Seconds
(without alignments)
11435.003 Million cell updates/sec

Title: US-10-018-105-3
Perfect score: 3525
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Scoring table: IDENTITY_NUC
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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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11: gb_sts.*
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13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3523	99.9	3525	6	BD273775 Identific
2	3523	99.9	3525	6	AX046919 Sequence
3	2769	78.6	2769	6	AX489375 Sequence
4	2155.2	61.1	2358	6	AR551197 Sequence
5	581	16.5	110000	8	Continuation (15 o
6	423.8	12.0	507	6	AR551196 Sequence
7	396	11.2	2580	8	AY692762 Saccharom
8	396	11.2	4202	8	SCY01130W
9	396	11.2	13421	8	SCY011293
10	385	10.9	110000	8	CR380951.1
11	383	10.9	270148	8	YSCCHRVIN
12	376	10.7	110000	8	CR382125_06
13	373.6	10.6	110000	8	AB016817_03
14	263.8	7.5	684	6	CQ446161
15	252.4	7.2	35030	8	SPBC37B12
16	252.4	7.2	38000	8	AB004539
17	252.4	7.2	38911	8	AB004538
18	215	6.1	110000	8	CR382130_00
19	191.2	5.4	43880	8	SPAC17G6
					Z99162 S.pombe chr

20	190.8	5.4	110000	8	CR382131_00	CR382131 Yarrowia
21	176.8	5.0	875	11	CNS06F3M	AL395912 T7 end of
c 22	172.4	4.9	163843	5	EX510939	EX510939 Zebrafish
c 23	172.4	4.9	211113	2	CR391962	CR391962 Danio rer
c 24	169.8	4.8	110000	8	CR380959_12	Continuation (13 o
c 25	168.2	4.8	537	6	AR5407	A85407 Sequence 66
c 26	168.2	4.8	537	6	AR154900	AR154900 Sequence
c 27	168.2	4.8	537	6	E65425	E65425 Genome DNA
c 28	150.6	4.3	110000	8	CR382137_08	Continuation (9 of
c 29	149	4.2	94534	5	AL929250	AL929250 Zebrafish
c 30	145.4	4.1	173019	5	EX321884	EX321884 Zebrafish
c 31	145	4.1	238084	2	EX950172	EX950172 Danio rer
c 32	144	4.1	34347	2	EX957360	EX957360 Danio rer
c 33	142.8	4.1	155204	2	AC007926	AC007926 Trypanoso
c 34	142	4.0	177575	5	AL953867	AL953867 Zebrafish
c 35	141.8	4.0	143342	2	CR388191	CR388191 Danio rer
c 36	140.2	4.0	145306	2	EX899179	EX899179 Danio rer
c 37	140.2	4.0	145553	5	AL935272	AL935272 Zebrafish
c 38	138.2	3.9	154071	3	AC115598	AC115598 Dictyoste
c 39	130.2	3.7	115990	5	EX890614	EX890614 Zebrafish
c 40	127.6	3.6	203127	5	EX322566	EX322566 Zebrafish
c 41	127.4	3.6	3957	8	SCYKL064W	ZX28064 S.cerevisia
c 42	127.4	3.6	28600	8	SCX1286K	X75781 S.cerevisia
c 43	126.8	3.6	100893	8	CR380959_13	Continuation (14 o
c 44	126.2	3.6	146415	5	AL929469	AL929469 Zebrafish
c 45	126.2	3.6	170800	2	CR352223	CR352223 Danio rer

ALIGNMENTS

RESULT 1	BD273775	3525 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD273775	3525 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	Identification of candida albicans essential antifungal drug discovery. and use thereof in antifungal drug discovery.				
ACCESSION	BD273775	1	GI:33083543		
VERSION	BD273775	1	GI:33083543		
KEYWORDS	JP 2002543799-A/2				
SOURCE	Candida albicans				
ORGANISM	Candida albicans				
REFERENCE	1	(bases 1 to 3525)			
AUTHORS	Roemer, T., Bussey, H. and Davison, J.				
TITLE	Identification of candida albicans essential antifungal specific genes and use thereof in antifungal drug discovery				
JOURNAL	Patent: JP 2002543799-A 2 24-DEC-2002;				
COMMENT	MC GILL UNIVERSITY				
	OS	Candida albicans			
	PN	JP 2002543799-A/2			
	PD	24-DEC-2002			
	PF	05-MAY-2000	JP 2000616385		
	PR	05-MAY-1999	US 60/132878		
	PI	TERRY ROEMER, HOWARD BUSSEY, JOHN DAVISON			
	PC	C12N15/09, C07K14/40, C07K16/14, C12Q1/68, G01N33/15, G01N33/50, PC			
	PC	G01N33/569			
	CC	Identification of candida albicans essential antifungal specific genes and use thereof in antifungal drug discovery			
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	FT	CDS	(338)..(3103).		
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ORIGIN					
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Best Local Similarity	100.0%; Pred. No. 0;
Matches 3525; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	1 TATATAATATAATATATAAACAATAACATATATAAAAAAACTTCATATTTTCAACTGTT 60
	1 TTTTTFSTFTSTFTSTFTATATATACATATATATAAAAACTTCATATTTTCAACTGTT 60

[illegible]

QY	818	AAATCAAGAGAAATCTCAATTTGGAAATTTACCTCCATTAATTAAGAAAGAAACAAAT	877	QY	1898	TATTTTGTGTTTCCATACCTTTTCAAGCTGATAAAGAAATCTGAAGATTAATTTAGAACCG	1957
DB	481	AAATCAAGAGAAATCTCAATTTGGAAATTTACCTCCATTAATTAAGAAAGAAACAAAT	540	DB	1561	TATTTTGTGTTTCCATACCTTTTCAAGCTGATAAAGAAATCTGAAGATTAATTTAGAACCG	1620
QY	878	GGTGGTAATTAATCTCAATTAATTTTGAATGATTTAGTTAGTCCCATGACAAATAATGAA	937	QY	1958	ATAAATGTTTATATTTGTTTCCATGATGATATTAACGTTCAATTTTCCACCAAT	2017
DB	541	GGTGGTAATTAATCTCAATTAATTTTGAATGATTTAGTTAGTCCCATGACAAATAATGAA	600	DB	1621	ATAAATGTTTATATTTGTTTCCATGATGATATTAACGTTCAATTTTCCACCAAT	1680
QY	938	ACTAATGATAGTGAAGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	997	QY	2018	TCTCATCCAGCAAAATGTTAGAAAGAGATTCGTCAATTCAGAGATTAATTCGATGTTAGT	2077
DB	601	ACTAATGATAGTGAAGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	660	DB	1681	TCTCATCCAGCAAAATGTTAGAAAGAGATTCGTCAATTCAGAGATTAATTCGATGTTAGT	1740
QY	998	ATTGGTGCTCAACCCCTGGTGGTGGAACTGGTACTACCGCCACTGCCACTGCCACTGCT	1057	QY	2078	GCTGATGTTGTTATGTTATGCTTAAATTCGATGAAATTAACGATGTTTGGCCCCGCTGAT	2137
DB	661	ATTGGTGCTCAACCCCTGGTGGTGGAACTGGTACTACCGCCACTGCCACTGCCACTGCT	720	DB	1741	GCTGATGTTGTTATGTTATGCTTAAATTCGATGAAATTAACGATGTTTGGCCCCGCTGAT	1800
QY	1058	GCTGCTGGTAGAGACCATCTCGTTCAATCTATGATAGTGAAGCTGATTTCTCATGCAATCA	1117	QY	2138	CATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2197
DB	721	GCTGCTGGTAGAGACCATCTCGTTCAATCTATGATAGTGAAGCTGATTTCTCATGCAATCA	780	DB	1801	CATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1860
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QY	1178	GTTAATGGAATTTGATGAAATTTGATGAAATTTTATAGAGAGAAAGAGAGAGCT	1237	QY	2258	AGATTTATCAGGTAAAGCTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2317
DB	841	GTTAATGGAATTTGATGAAATTTGATGAAATTTTATAGAGAGAAAGAGAGAGCT	900	DB	1921	AGATTTATCAGGTAAAGCTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1980
QY	1238	TATTTACAAACAAATGCTTAAATTAATTTCTGCTATGATGATTAATTAATTAATTAATTAAT	1297	QY	2318	GCTAATTTCTTCTGTTGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2377
DB	901	TATTTACAAACAAATGCTTAAATTAATTTCTGCTATGATGATTAATTAATTAATTAATTAAT	960	DB	1981	GCTAATTTCTTCTGTTGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2040
QY	1298	TCCAAAATAATATCTACTAGTGGTGCATCTCGTCAATCCATATCATCATCATCATCATCAT	1357	QY	2378	GCCCCACCCACCCACCTAATCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2437
DB	961	TCCAAAATAATATCTACTAGTGGTGCATCTCGTCAATCCATATCATCATCATCATCATCAT	1020	DB	2041	GCCCCACCCACCCACCTAATCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2100
QY	1358	AATAAATAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1417	QY	2438	AATAGTTTAGGAACTTCAACTGGTGGAGGAGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2497
DB	1021	AATAAATAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1080	DB	2101	AATAGTTTAGGAACTTCAACTGGTGGAGGAGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2160
QY	1418	CCAAAATAATTTTAAAGAAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1477	QY	2498	AATCCAACTGAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2557
DB	1081	CCAAAATAATTTTAAAGAAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1140	DB	2161	AATCCAACTGAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2220
QY	1478	TCCTCAGAGAAATTTATGAAATGAAGACTAAACCAACACACCTTACAAATATGATGAT	1537	QY	2558	CAACAAACCAACCAACATGTTATCACTAAACAAATCTTTCCCAATCCCGATGACGTCCA	2617
DB	1141	TCCTCAGAGAAATTTATGAAATGAAGACTAAACCAACACACCTTACAAATATGATGAT	1200	DB	2221	CAACAAACCAACCAACATGTTATCACTAAACAAATCTTTCCCAATCCCGATGACGTCCA	2280
QY	1538	CAATTAATCAATTAATCAATCTTCTAATCTTGGATCTGGATCTGGGAGGTGAA	1597	QY	2618	AGAGCTGATATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2677
DB	1201	CAATTAATCAATTAATCAATCTTCTAATCTTGGATCTGGATCTGGGAGGTGAA	1260	DB	2281	AGAGCTGATATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2340
QY	1598	TTTGGTGGAGCAAGAAATTTCTGATGGAATTAATGAGGTTTCAATCTGATAGATTTTCA	1657	QY	2678	AATTTATTTAGCTATGAAATAATTTTCACTGCTTCACTTCACTTCACTTCACTTCACTTCACT	2737
DB	1261	TTTGGTGGAGCAAGAAATTTCTGATGGAATTAATGAGGTTTCAATCTGATAGATTTTCA	1320	DB	2341	AATTTATTTAGCTATGAAATAATTTTCACTGCTTCACTTCACTTCACTTCACTTCACTTCACT	2400
QY	1658	CTTTTCCATCTGAATCAGAGAAATCTATTTCAATGCCCCCGATATCCATCATTTAGTATCA	1717	QY	2738	CAAGTTGATCAATCAATTTCCAAATTAATAAATCACCGAAATGTTTTCTAAATTAATTTG	2797
DB	1321	CTTTTCCATCTGAATCAGAGAAATCTATTTCAATGCCCCCGATATCCATCATTTAGTATCA	1380	DB	2401	CAAGTTGATCAATCAATTTCCAAATTAATAAATCACCGAAATGTTTTCTAAATTAATTTG	2460
QY	1718	CCAGGTCAATCTCTGTCGAGATTTTATTTAGAAATGGTGAAGAACTTGGTGGTGGTGGTGGT	1777	QY	2798	ATTGGGCAATGTTAGTTTCCATTAATTTAGTCAAGGACTTTTGGTATGATGATGATGATGATGAT	2857
DB	1381	CCAGGTCAATCTCTGTCGAGATTTTATTTAGAAATGGTGAAGAACTTGGTGGTGGTGGTGGT	1440	DB	2461	ATTGGGCAATGTTAGTTTCCATTAATTTAGTCAAGGACTTTTGGTATGATGATGATGATGATGAT	2520
QY	1778	ACTTGTCTACTGATTCGAAATGAATAATGTTGGCCAAAGCAATTTGGTATTTCACTCTTTA	1837	QY	2858	GTCCCTGGTGAAGGTTGATCAATTTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	2917
DB	1441	ACTTGTCTACTGATTCGAAATGAATAATGTTGGCCAAAGCAATTTGGTATTTCACTCTTTA	1500	DB	2521	GTCCCTGGTGAAGGTTGATCAATTTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	2580
QY	1838	ACTGCTCAAGATTTCCAAATGCAAGAACTGCTGAAAGAGTTGAAATTAATTTAAAGATTTAT	1897	QY	2918	TTTATTAATTTAGGATCAATTTATTTATTTGCTCAATGTTGTTGAAAAAATTTGAATTAATTTCA	2977
DB	1501	ACTGCTCAAGATTTCCAAATGCAAGAACTGCTGAAAGAGTTGAAATTAATTTAAAGATTTAT	1560	DB	2581	TTTATTAATTTAGGATCAATTTATTTATTTGCTCAATGTTGTTGAAAAAATTTGAATTAATTTCA	2640
				QY	2978	ATTGAAGGCAAAATTAATTTAGTGAATTCGACCAATTTTAAATCAATTCATCAAGAGATCAAT	3037

QY		813	CTAATAAAATCAAGAAGAAAAATCTCAAATTGGGAAAATTTTACCCTCCATTAATTTAAAGAGAAA	872
Dd		539	CTAATAAAATCAAGAAGAAAAATCTCAAATTGGGAAAATTTTACCCTCCATTAATTTAAAGAGAAA	598
QY		873	CAATTGGTGCGTAATAAATCTTAATAAATTTTGAAAATGAATTTAGTAGTCCTCATACATAATGA	932
Dd		599	CTAATTGGTGCGTAATAAATCTTAATAAATTTTGAAAATGAATTTAGTAGTCCTCATACATAATGA	658
QY		933	TGAAAACCTAATGATAGTAGGAAGATATTACTAA-----TACTAGCACCACTGTCTAATCATATGA	989
Dd		659	TGAAAACCTAATGATAGTAGGAAGATATTACTAATACTACTAGCACCACTGTCTAATCATATGA	718
QY		990	AAC TTGGTATTTGGTGCTACAACCCCTTGGTGTTGGAACTGGTACTACGCCACACTGCCACTG	1049
Dd		719	AAC TTGGTATTTGGTGCTACAACCCCTTGGTGTTGGAACTGGTACTACGCCACACTGCCACTG	778
QY		1050	CCACTGCTGCTGC-----TGGTAGAGAACCACTCTCGTTCACTCTATTTGATPAGTGAAG	1100
Dd		779	CCA CTGCTACTGCTGGTGTTGGTGTAGAGAACCACTCTCGTTCACTCTATTTGATPAGTGAAG	838
QY		1101	CTGAATCTCATGATCAAGATCATCTCAAGAACTCAAGAAAGTGTGTCTGTTTTCCTATG	1160
Dd		839	CTGAATCTCATGATCAAGATCATCTCAAGAACTCAAGAAAGTGTGTCTGTTTTCCTATG	898
QY		1161	TTGGTGATCATATTAGAGTTAATGGAAATTCATTTTTGATGAAATTTGATGAATTTATTAGAG	1220
Dd		899	TTGGTGATCATATTAGAGTTAATGGAAATTCATTTTTGATGAAATTTGATGAATTTATTAGAG	958
QY		1221	AAGAAAGAGAGAGCTTATTTACAAAAACAAATGANTGCTAAAAATATTTCTGCGTATTG	1280
Dd		959	AAGAAAGAGAGAGCTTATTTACAAAAACAAATGANTGCTAAAAATATTTCTGCGTATTG	1018
QY		1281	ATGAATTTCAAATCTTTCCAAAAATAATACTACTAGTGGTGCGATCTCGTCATCCATATC	1340
Dd		1019	ATGAATTTCAAATCTTTCCAAAAATAATACTACTAGTGGTGCGATCTCGTCATCCATATC	1078
QY		1341	ATCATCACAGTAAATAATAAAAAATAATGGTGGTGATG---GTGGTGCTCTAGTA	1397
Dd		1079	ATCATCACAGTAAATAATAAAAAATAATGGTGGTGATG---GTGGTGCTCTAGTA	1138
QY		1398	TGGCAGCATTTAAATATATCTCCAAAAATATTTTAAAGAAAACATTTACAAGATTGGAAT	1457
Dd		1139	TGGCAGCATTTAAATATATCTCCAAAAATATTTTAAAGAAAACATTTACAAGATTGGAAT	1198
QY		1458	TTACTCATGAAAATCTTCATCTTCAGAGAAATTTATGAATTTGAAGACTAAACAACAC	1517
Dd		1199	TTACTCATGAAAATCTTCATCTTCAGAGAAATTTATGAATTTGAAGACTAAACAACAC	1258
QY		1518	GACCTTACAAATATGATGATCAATTTATCAATTAACCTTCATCTATCATCTTCTACT-----T	1571
Dd		1259	CACCTTACAAATATGATGATCAATTTATCAATTAACCTTCATCTATCATCTTCTCGGAT	1318
QY		1572	CTGGATCTGGATCTGGCAGGTGAAATTTGGTGGAGCAAGAAATTTCTGATGGGATTAATG	1631
Dd		1319	CTGGATCTGGATCTGGCAGGTGAAATTTGGTGGAGCAAGAAATTTCTGATGGGATTAATG	1378
QY		1632	GAGGTTCAATCTCATAGATTTTCACCTTTTCCATCTCTGAAATCAGAGAAACTATTTCATG	1691
Dd		1379	GAGGTTCAATCTCATAGATTTTCACCTTTTCCATCTCTGAAATCAGAGAAACTATTTCATG	1438
QY		1692	CCCCCGATATTCATCATTTAGTATCACAGGTCAATCTGTTTCGAGATTTATTTTAGMAATG	1751
Dd		1439	CCCCCGATATTCATCATTTAGTATCACAGGTCAATCTGTTTCGAGATTTATTTAGMAATG	1498
QY		1752	GTGAAGAAACTTGGTGGTTAGATTGTACTTGCTCTTACATGATTCGGAAATGAAAATGTGG	1811
Dd		1499	GTGAAGAAACTTGGTGGTTAGATTGTACTTGCTCTTACATGATTCGGAAATGAAAATGTGG	1558
QY		1812	CCAAAGCAATTTGGTATTTCATCTTTTAACTGCTGAAGATTTTCGAATCGAGAACTCGTG	1871
Dd		1559	CCAAAGCAATTTGGTATTTCATCTTTTAACTGCTGAAGATTTTCGAATCGAGAACTCGTG	1618
QY		1872	AAAAAGTTGAATTTATTTAAAGTTATTTATTTTGTGTTTCTCCATCTTTTGAAGCTGATA	1931

Db	1619	AAAAAGTTGAAATATATATATAAGTTATATATTTGGTTGTTTCCATCTTTGAGCTGATA	1678
Qy	1932	AAGAACTCTGAAGATATATATAGAACCGATAAATGTTTATATATGTTGTTTCCATGATGTA	1991
Db	1679	AAAACTGAGATATATATAGAACCGATAAATGTTTATATATGTTGTTTCCATGATGTA	1738
Qy	1992	TATTAACGTTTCATTTTCCAAATTTCTATCCAGCAAAATGTTTGAAGAGAGTTCTCTC	2051
Db	1739	TATTAACGTTTCATTTTCCAAATTTCTATCCAGCAAAATGTTTGAAGAGAGTTCTCTC	1798
Qy	2052	AAATGAGAGATATATGTCGATGTTAGTGTGTTATGTTATGTTTAAATCCGATGAAA	2111
Db	1799	AAATGAGAGATATATGTCGATGTTAGTGTGTTATGTTATGTTTAAATCCGATGAAA	1858
Qy	2112	TTACCGATGTTTGGCCCGGCTGATTCATGGAATTTGAATATGAAGCTGATGCCATGGAAG	2171
Db	1859	TTACCGATGTTTGGCCCGGCTGATTCATGGAATTTGAATATGAAGCTGATGCCATGGAAG	1918
Qy	2172	ATGCGGTTTTCATCTGATGATATCTGATTTTAGTATGTTTACAAAGATTTGGTGAAT	2231
Db	1919	ATGCGGTTTTCATCTGATGATATCTGATTTTAGTATGTTTACAAAGATTTGGTGAAT	1978
Qy	2232	CAAGAAGAAAGTCATGCTTTTAAATCAGATTTATTCAGTAAAGCTGATGTCATTAATAA	2291
Db	1979	CAAGAAGAAAGTCATGCTTTTAAATCAGATTTATTCAGTAAAGCTGATGTCATTAATAA	2038
Qy	2292	TGTTTCTTAAAGATCTCAAGAAAGCTAAATTTCTTCTGTTTATTAATCAACGTCAT	2351
Db	2039	TGTTTCTTAAAGATCTCAAGAAAGCTAAATTTCTTCTGTTTATTAATCAACGTCAT	2098
Qy	2352	ATAACTTCAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC	2405
Db	2099	ATAACTTCAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC	2158
Qy	2406	TTACTTCCCAATTAATCAACTTCAACTTCAACTTCAACTTCAACTTCAACTTCAACTTCA	2465
Db	2159	TTACTTCCCAATTAATCAACTTCAACTTCAACTTCAACTTCAACTTCAACTTCAACTTCA	2218
Qy	2466	GAGTAGGAGTAGGAGGAAATTAATTTTGGTCCCAATCCAACTGGAATAATACTAATACTA	2525
Db	2219	GAGTAGGAGTAGGAGGAAATTAATTTTGGTCCCAATCCAACTGGAATAATACTAATACTA	2278
Qy	2526	ATACTAATACTACTGTTTCACTTCACTCACTCACTCACTCACTCACTCACTCACTCACTA	2585
Db	2279	ATACTAATACTACTGTTTCACTTCACTCACTCACTCACTCACTCACTCACTCACTCACTA	2335
Qy	2586	ACAAATCTTTCCCATCCCC	2605
Db	2336	ACAAATCTTTCCCATCCCC	2355

RESULT 5
CR382138_14/c
WPCOMMENT
Sequence split into 24 fragments LOCUS CR382138 Accession CR382138

Fragment Name	Begin	End
CR382138_00	1	110000
CR382138_01	100001	210000
CR382138_02	200001	310000
CR382138_03	300001	410000
CR382138_04	400001	510000
CR382138_05	500001	610000
CR382138_06	600001	710000
CR382138_07	700001	810000
CR382138_08	800001	910000
CR382138_09	900001	1010000
CR382138_10	1000001	1110000
CR382138_11	1100001	1210000
CR382138_12	1200001	1310000
CR382138_13	1300001	1410000
CR382138_14	1400001	1510000
CR382138_15	1500001	1610000

CR382138_16	1600001	1710000
CR382138_17	1700001	1810000
CR382138_18	1800001	1910000
CR382138_19	1900001	2010000
CR382138_20	2000001	2110000
CR382138_21	2100001	2210000
CR382138_22	2200001	2310000
CR382138_23	2300001	2336804
Continuation (15 of 24) of CR382138 from base 1400001 (CR382138 Debaryomyces hansenii chi		
Query Match 16.5%; Score 581; DB 8; Length 110000;		
Best Local Similarity 58.1%; Pred. No. 1.9e-72;		
Matches 1348; Conservative 0; Mismatches 815; Indels 158; Gaps 12;		
Qy	1067	AGAAGACCATCTCGTTCATCTATTGATAGTAGTGAAGCTGATTTCTCATGATCAAGATCATCT 1126
Db	14194	AGAAGACCATCTCGTTCATCTATTGATAGTAGTGAAGCTGATTTCTCATGATCAAGATCATCT 14135
Qy	1127	CAAGAACTGAAGAGATGTTTGTTCCTATGTTGGTGGTATCATATTAGAGTTAATGGA 1186
Db	14134	CAGGAGACAGAAGAGATGTTTGTTCCTATGTTGGTGGTGAACACGTTTCGGTGTAAAGGGT 14075
Qy	1187	ATTGATTTTGTGATGAATTTGATGAAATTTATTATAGAGA--AGAAGAGAGAAGAGCTTATTAT 1244
Db	14074	ATTGATTTTGTGATGAATTTGATGAAATTTATTATAGAGA--AGAAGAGAGAAGAGATGAATGCA 14015
Qy	1245	AAAAAAATGATCTCTAAAAAATATTCTGCGTATTGATGAATTTCCAAATCTTTCCAAA 1304
Db	14014	AAAGAGAAACACAGATGATCGCAGAAAGAACAGCCATGAGGGT-----TGATACCTGGAC 13960
Qy	1305	ATAATPACTAGTGGTGGTCTCTGTCATCCATATCATCATCATCATCATCATCATCATCATCAT 1364
Db	13959	ATGGGAGTGGCGCGCATGTAGTGC--CCAGTAAAAATGCCTTGAAAAATATATCTCCGTCAAA 13901
Qy	1365	AAAATAATGGTGGTGGTCTCTGATGTCGAGCA--TAAATAATATATCTCCAAA 1424
Db	13900	ATATTAGGAAAGGCTTCGTTTCGAAAGTTTGGTAGAAGAAATACCTTACGAGGAGACATA 13841
Qy	1425	ATATTAAAGAAACATTTATCAAGATTTGAATTTTATCTCATGAAATCTTTCATCTTCAG 1484
Db	13840	ATGCTCTTATCTGTTATTAAT--ATTTCGAGAGGAGCACAATCAGATTTCTTCTACCGTTA 13783
Qy	1485	AAGAAATTTATGAATGAAGACTAAACAAACACACCTTACAAATATGATGATCAATTTAT 1544
Db	13782	CAGATGATTTCTGCTCTAGGAGATACACGAAAGATTTTGGGAGACGATGATTTTCGA 13723
Qy	1545	CATTAATCTTACTACATCTTCTACTTCTGGATCTGATCTGGGAGGTGAAATTTGGTG 1604
Db	13722	CCGAAA-----ATGTTAAGTTTGGTG 13702
Qy	1605	GAGCAAGAAATTTCTGATGGATTTAATGAGAGTTTCACTACCTGATAGATTTTCACTTTTCC 1664
Db	13701	GTACAAGAAATCAACGA-----TATGATTCGGCATTCGCTGAAAGGTTTTCATCTTTT 13648
Qy	1665	ATTCTGAATCAGAAGAAATTTATTCATGCCCCCATTTTCATCATTTAGTATCACAGGTC 1724
Db	13647	GTTCCGAAATCAGAAGAAACAAATACATGCTCTCATATTCCTTCTGTTGGTCAAACTGGGC 13588
Qy	1725	AATCTGTTGGAGATTTTATTAGAAATGGTGAAGAACTTGGTGGTGGTATGTTGTTTGTG 1784
Db	13587	AGAGTGTGAAGCGATTTTGTTCAGAAATGGTGAAGTACATGGTGGCTTGAATTTGTTTGGC 13528
Qy	1785	CTACTGATTCGGAATGAAATTTGTCGCAAAAGCATTTGGTATTCATCTTCACTTTAATCTGT 1844
Db	13527	CTACTGATGCTGAATGAAATTTGTTGCTAAAGCATTTGGTATTCATCTTCACTTTGACAGCTG 13468
Qy	1845	AAGATATTTCGAATGCAAGAACTCGTGAAGAAAGTTGAATTTATTAAAAAGTTATTATTG 1904
Db	13467	AGATATTTCGATGCAAGAAACCGTGAAGAAAGTTGAATTTATTAAAAAGTTATTATTG 13408
Qy	1905	TTTGTTCCTATACTTTTGAAGCTGATGAAGATCTGAAGATTTATTTAGAACCGGATAATG 1964
Db	13407	TTTGTTCCTATACTTTTGAAGCTGATGAAGATCTGAAGATTTATTTAGAACCGGATAATG 13348

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 14:15:33 ; Search time 10845 Seconds
(without alignments)
12372.204 Million cell updates/sec

Title: US-10-018-105-3

Perfect score: 3525

Sequence: 1 tatataatataatatata.....tcaattattcaattattgc 3525

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: gb_est1.*

2: gb_est2.*

3: gb_est3.*

4: gb_est4.*

5: gb_est5.*

6: gb_est6.*

7: gb_est7.*

8: gb_est8.*

9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	359.8	10.2	912	9	AL399925 T7 end of
C 2	301.6	8.6	1032	9	AL427134 clone BA0
C 3	211.2	6.0	1089	9	AL410742 T3 end of
C 4	210.8	6.0	798	9	AL426171 clone BA0
C 5	202	5.7	579	8	BZ295013 CG1236.f1
C 6	187.2	5.3	911	9	AL399045 T3 end of
C 7	176	5.0	874	9	AL398239 T3 end of
C 8	176	5.0	911	9	AL397913 T3 end of
C 9	172.4	4.9	955	7	CO028936 EST807320
C 10	163	4.6	387	7	CO142543
C 11	156.2	4.4	771	7	CF709049 CCAGA79TF
C 12	146	4.1	973	9	CNS06GSK
C 13	145.4	4.1	524	8	BZ297820 CG3653.r1
C 14	143	4.1	763	1	AJ637812
C 15	141.2	4.0	614	4	BM266292 VL58 cdNA
C 16	141	4.0	712	5	BQ743184
C 17	133.2	3.8	964	7	CO034119
C 18	128.4	3.6	850	6	CD488559
C 19	122.6	3.5	850	9	CNS06X53
C 20	121.8	3.5	921	9	CNS07592
C 21	119.2	3.4	907	7	CO027928
C 22	117	3.3	895	9	CNS06HJ7
C 23	114.8	3.3	934	7	CF823927
C 24	110.2	3.1	551	1	AJ637804

C 25	109.4	3.1	786	7	CF709038
C 26	108.6	3.1	1061	9	CNS07DEE
C 27	108.2	3.1	901	7	CO011480
C 28	108	3.1	965	7	CF820256
C 29	106.6	3.0	641	8	AQ946120
C 30	106	3.0	575	8	BZ780846
C 31	102.4	2.9	819	7	CF715298
C 32	102.2	2.9	707	9	CG403581
C 33	100.6	2.9	815	7	CO025755
C 34	100.6	2.9	823	7	CO025396
C 35	100.6	2.9	907	7	CO028288
C 36	100.6	2.9	932	7	CO025732
C 37	100.6	2.9	936	7	CO031086
C 38	100.6	2.9	989	7	CO028935
C 39	100.4	2.8	413	5	BQ491813
C 40	99.8	2.8	587	8	BH873429
C 41	99.8	2.8	781	9	BX145762
C 42	97.4	2.8	832	8	BH391984
C 43	96.2	2.7	772	7	CF816703
C 44	96	2.7	700	8	AQ940248
C 45	95.4	2.7	670	8	BZ388480

ALIGNMENTS

RESULT 1
CNS06173/c
LOCUS
DEFINITION
T7 end of clone AS0AA018C10 of library AS0AA from strain CLIB 533
of Saccharomyces bayanus, genomic survey sequence.
ACCESSION
AL399925
VERSION
AL399925.1 GI:12155087
KEYWORDS
GSS.
SOURCE
Saccharomyces bayanus
ORGANISM
Saccharomyces bayanus
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
REFERENCE
1 (bases 1 to 912)
Souciet J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Maupertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P., and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)

JOURNAL
MEDLINE
PUBMED
REFERENCE
2 (bases 1 to 912)
Bon, E., Neuveglise, C., Casaregola, S., Artiguenave, F., Wincker, P.,
Aigle, M., and Durrens, P.
Genomic exploration of the hemiascomycetous yeasts: 5.
Saccharomycetes bayanus var. uvarum
FEBS Lett. 487 (1), 37-41 (2000)
JOURNAL
MEDLINE
PUBMED
REFERENCE
3 (bases 1 to 912)
Genoscope.
Direct Submission
Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomycetes
exiguus, Saccharomycetes servazzii, Zygosaccharomyces rouxii,
Saccharomycetes kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbicola,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	2769	78.6	2769	16	US-10-032-585-6675	Sequence 6675, Ap
2	179.6	5.1	1992	15	US-10-128-714-2563	Sequence 2563, Ap
3	179.6	5.1	1992	15	US-10-128-714-7563	Sequence 7563, Ap
4	118	3.3	462	11	US-09-864-4083-2265	Sequence 2265, Ap
5	117.6	3.3	8056	18	US-10-473-128-386	Sequence 386, App
6	116.4	3.3	688	18	US-10-653-047-7103	Sequence 7103, Ap
7	113.6	3.2	2048	15	US-10-128-714-1563	Sequence 1563, Ap
8	113.6	3.2	2048	15	US-10-128-714-6563	Sequence 6563, Ap
9	113.6	3.2	4048	15	US-10-128-714-563	Sequence 563, App
10	113.6	3.2	4048	15	US-10-128-714-5563	Sequence 5563, Ap
c. 11	106.8	3.0	4985	14	US-10-094-240-10	Sequence 10, App1

QY 2678 AATTATTAGCTATGAAAAATTTTCAGTCGTTCCACATTCAAAATTATTAGCTCAATTA 2737
 DB 2341 AATTATTAGCTATGAAAAATTTTCAGTCGTTCCACATTCAAAATTATTAGCTCAATTA 2400
 QY 2738 CAAGTTGAATCAATTCAAATTCCAATAATAAAATCACCGAAATGTTTTTCAAAAATTACTTTG 2797
 DB 2401 CAAGTTGAATCAATTCAAATTCCAATAATAAAATCACCGAAATGTTTTTCAAAAATTACTTTG 2460
 QY 2798 ATTGGGCAATGTTAGTTCCATTAATTTAGTCACGGGACATTTTGGGTATGAATGAAGA 2857
 DB 2461 ATTGGGCAATGTTAGTTCCATTAATTTAGTCACGGGACATTTTGGGTATGAATGAAGA 2520
 QY 2858 GTCCCTGCTGAGGCTGACCAATTTAGTGTGTTTTTCCGGAATGTTGGAGTATTAATA 2917
 DB 2521 GTCCCTGCTGAGGCTGACCAATTTAGTGTGTTTTTCCGGAATGTTGGAGTATTAATA 2580
 QY 2918 TTATTAATTTATGGAATCAATTTATATTTGCTCAATGCTGTTGAAAAAATTCGAATAATCA 2977
 DB 2591 TTATTAATTTATGGAATCAATTTATATTTGCTCAATGCTGTTGAAAAAATTCGAATAATCA 2640
 QY 2978 ATTGAAGCAAAAATTAATGTAATCGACCAATTTTATTAATCAATTCATCAAGAAATCAAT 3037
 DB 2641 ATTGAAGCAAAAATTAATGTAATCGACCAATTTTATTAATCAATTCATCAAGAAATCAAT 2700
 QY 3038 AGAAGTTAGTTTAAAAAATCATGCTGTTAATCAATCAATTTAGTTTCCCAATAAA 3097
 DB 2701 AGAAGTTAGTTTAAAAAATCATGCTGTTAATCAATCAATTTAGTTTCCCAATAAA 2760
 QY 3098 TATGAATAA 3106
 DB 2761 TATGAATAA 2769

RESULT 2

US-10-128-714-2563
 ; Sequence 2563, Application US/10128714
 ; Publication No. US20030119013A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jiang, Bo
 ; APPLICANT: Hu, Wengqi
 ; APPLICANT: Tishkoff, Daniel
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Lemieux, Sebastien M
 ; APPLICANT: Eroshkin, Alexey M
 ; TITLE OF INVENTION: Identification of Essential Genes in *Aspergillus fumigatus* and
 ; TITLE OF INVENTION: Methods of Use
 ; FILE REFERENCE: 10182-018-999
 ; CURRENT APPLICATION NUMBER: US/10/128,714
 ; PRIOR FILING DATE: 2002-04-23
 ; PRIOR APPLICATION NUMBER: US 60/285,697
 ; PRIOR FILING DATE: 2001-04-23
 ; PRIOR APPLICATION NUMBER: US 60/287,066
 ; PRIOR FILING DATE: 2001-04-27
 ; PRIOR APPLICATION NUMBER: US 60/295,890
 ; PRIOR FILING DATE: 2001-06-05
 ; PRIOR APPLICATION NUMBER: US 60/303,899
 ; PRIOR FILING DATE: 2001-07-09
 ; PRIOR APPLICATION NUMBER: US 60/316,362
 ; PRIOR FILING DATE: 2001-08-31
 ; NUMBER OF SEQ ID NOS: 8603
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2563
 ; LENGTH: 1992
 ; TYPE: DNA
 ; ORGANISM: *Aspergillus fumigatus*
 US-10-128-714-2563

Query Match 5.1%; Score 179.6; DB 15; Length 1992;
 Best Local Similarity 56.6%; Pred. No. 3e-20;
 Matches 376; Conservative 0; Mismatches 279; Indels 9; Gaps 2;
 QY 1659 TTTTCCATTTCTGAATCAGAAAGAACTATTTCATGCCCCCGATATTCATCATATTAGTATCAC 1718

DB 959 TTTTCTCATCCGAGTCCAGAGCACTGTGCATCGCGGGAATCGGGGACCTTTGTGCTCC 1018
 QY 1719 CAGTGCATCTGTTCGAGATTTATTAGAAATGG-----TGAAGAAACTTTGGTGGTTAG 1772
 DB 1019 CTGCTGATCTCTTCGCGGATCTCTTTCACATTCGCGGAGGAGGTGTGTGGTGGTTGG 1078
 QY 1773 ATTGTACTTGTCTTACTGATTCGGAAATGAAATGTTGGCCAAAGCATTTTGGTATTTCATC 1832
 DB 1079 ACGTACTCAATCCAAACAGAGGAGGAGTGTGCTGCATCTTCGCGGCAATTTTCCATCCATC 1138
 QY 1833 CTTTAACTGCTTGAAGATATTTCGAATGCAAGAAACTCGTGAAGAAAGTTTGAATTTATTAATA 1892
 DB 1139 CACTGACTACGGAAGATATCTTGACTCAAGAAGCCCGTGAAGAGGTGAGCTTTTCAAGC 1198
 QY 1893 GTTATTAATTTTGTGTTTGTTCATTAATTTT---TGAAGCTGATAAAGATCTCGAAGATATT 1949
 DB 1199 AATATTACTTTGTCTGCTTCGCGACATTTCTATCAGCTCGCAAGACAGACGACGCTTCA 1258
 QY 1950 TAGAACCGATAAATGTTTATATTTGCTGTTTCCATGATGTTATTAACGTTCCATTTT 2009
 DB 1259 TGGAGCCCGTCACTCTTACATGTTGTTTCCCGACGGTGTCTCTCATTTCTCATTTCA 1318
 QY 2010 CACCAATTTCTCATCCAGCAAAATGTTAGAAGAGAGTTTCTCAATTCGAGAGATTTATGTCG 2069
 DB 1319 CCGAGATCCACACCGCGCAATGTCAGGAAGAGAAATTTGGGAAGCTTCGTGATTTGTT 1378
 QY 2070 ATGTTAGTGTGATGTTGTTATGTTTATGCTTAAATTCGATGAATTAACGATGTTTGGCCC 2129
 DB 1379 CCCTCAGTAGTACTGATCTGTTATGCCATGATTCAGACATTTGTTGATAGTTTGGGC 1438
 QY 2130 CCGTGAATTCAGGAATTCGAATATGAAGCTGATGCCATTCAGATGCGGTTTTCCTACTGCTA 2189
 DB 1439 CTGTCATCCGAGAGATTCGATTCGAATCTGAGGCAATTCGAGGACCTCGTTTTCATCGCGC 1498
 QY 2190 GAGATACTGATTTTATGATGTTTACAAAGAAATGTTGTAATCAAGAAAGAAAGTCATGA 2249
 DB 1499 CGCTCGAGATTTTGAATCTCTTACCGGAATCGTGGGCTTCGTAAGAGGTCATGA 1558
 QY 2250 CTTTAAATGAGATTTATTCAGGTTAAGCTGATGCTATTAATAATGTTTGTCTAAAGATGTC 2309
 DB 1559 GCTTGTAGCGCTTCTAGGTGGCAAGCAGATGTCATTCGGGGTTTCTTCAAGCGTTTCA 1618
 QY 2310 AAGA 2313
 DB 1619 ACGA 1622

RESULT 3

US-10-128-714-7563
 ; Sequence 7563, Application US/10128714
 ; Publication No. US20030119013A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jiang, Bo
 ; APPLICANT: Hu, Wengqi
 ; APPLICANT: Tishkoff, Daniel
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Eroshkin, Alexey M
 ; APPLICANT: Lemieux, Sebastien M
 ; TITLE OF INVENTION: Identification of Essential Genes in *Aspergillus fumigatus* and
 ; TITLE OF INVENTION: Methods of Use
 ; FILE REFERENCE: 10182-018-999
 ; CURRENT APPLICATION NUMBER: US/10/128,714
 ; PRIOR FILING DATE: 2002-04-23
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 ; PRIOR FILING DATE: 2001-04-23
 ; PRIOR APPLICATION NUMBER: US 60/287,066
 ; PRIOR FILING DATE: 2001-04-27
 ; PRIOR APPLICATION NUMBER: US 60/295,890
 ; PRIOR FILING DATE: 2001-06-05
 ; PRIOR APPLICATION NUMBER: US 60/303,899
 ; PRIOR FILING DATE: 2001-07-09
 ; PRIOR APPLICATION NUMBER: US 60/316,362